<110>   Edgar B. Cahoon
        Howard G. Damude
        William D. Hitz
        Anthony J. Kinney
        Charles W. Kolar
        Zhan Bin Liu

<120>   Production of Long Chain Polyunsaturated Fatty Acids in Plants

<130>   BB1538 US NA

<140>
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<150>   US 60/446,941
<151>   2003-02-12

<160>   98

<170>   PatentIn version 3.2

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Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
        50   55   60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
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Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
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                100   105   110

Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
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Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
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Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
145   150   155   160

Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
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His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
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Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
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His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
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Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
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Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
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Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
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9

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Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
            325   330   335

Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His
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Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
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Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
385   390   395   400

Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
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<213> Saprolegnia diclina

<400> 36
Met Val Gln Gly Gln Lys Ala Glu Lys Ile Ser Trp Ala Thr Ile Arg
1   5   10   15

Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val
                20   25   30

Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
            35   40   45

Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
        50   55   60

Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
65   70   75   80

Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
                85   90   95

Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
            100   105   110

Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
        115   120   125

Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu
    130   135   140

His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly
145   150   155   160

Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His
                165   170   175

Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val
            180   185   190

Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His
        195   200   205

Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala
    210   215   220

Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser
225   230   235   240

Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe
                245   250   255

Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg
            260   265   270

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Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly
        275   280   285

Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala
        290   295   300

Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala
305   310   315   320

Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala
            325   330   335

Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly
            340   345   350
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln
            355   360   365

Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe
        370   375   380

Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val
385   390   395   400

Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys
            405   410   415

Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met
            420   425   430

Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys
            435   440   445

Glu Phe Pro Ala Met
        450

<210>   37
<211>   1413
<212>   DNA
<213>   Saprolegnia diclina

<400>   37
atggccccgc agacggagct ccgccagcgc cacgccgccg tcgccgagac gccggtggcc   60
ggcaagaagg cctttacatg gcaggaggtc gcgcagcaca acacggcggc ctcggcctgg   120
atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc   180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga ctcgtaccac   240
ccgttcagcg acaaggccga tcgatcttg aacaagtatg agattggcac gttcacgggc   300
ccgtccgagt tccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc   360
gttggcgagt acttcaagaa gaacaacctc atccgcagg acggcttccc gggcctctgg   420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact   480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg   540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac   600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac   660
cagcacgtcg tgggccacca catctacacg aacgtcgcgg gctcggaccc ggatcttccg   720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac   780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc   840
caggacttca ccgacacgtt cggctcgcac acgaacggcc gatccgcgt caacccgcac   900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg   960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc   1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc   1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc   1140

12

```
tcgcaggtca agacgtcggt cgactacgcc catggctcgt ggatgacgac gttccttgcc    1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac    1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc    1320
ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag    1380
cagggcatcg ccgccacgat ccacatgggc taa                                 1413
```

<210>   38
<211>   470
<212>   PRT
<213>   Saprolegnia diclina

<400>   38

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Met Ala Pro Gln Thr Glu Leu Arg Gln Arg His Ala Ala Val Ala Glu
1               5                  10                  15

Thr Pro Val Ala Gly Lys Lys Ala Phe Thr Trp Gln Glu Val Ala Gln
            20                  25                  30

His Asn Thr Ala Ala Ser Ala Trp Ile Ile Ile Arg Gly Lys Val Tyr
        35                  40                  45

Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val
    50                  55                  60

Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His
65                  70                  75                  80

Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly
                85                  90                  95

Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly
            100                 105                 110

Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn
        115                 120                 125

Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val
    130                 135                 140

Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr
145                 150                 155                 160

Ile Phe Ala Leu Gln Leu Ala Ala Ala Ala Leu Phe Gly Val Cys Gln
                165                 170                 175

Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr
                180                 185                 190

Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp
        195                 200                 205

Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val
    210                 215                 220

Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro
225                 230                 235                 240

Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe
                245                 250                 255
```

13

```
Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly
            260                 265                 270

Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly
            275                 280                 285

Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr
    290                 295                 300

Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val
305                 310                 315                 320

Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala
                325                 330                 335

Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn
            340                 345                 350

Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp
            355                 360                 365

Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys
    370                 375                 380

Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met Thr Thr Phe Leu Ala
385                 390                 395                 400

Gly Ala Leu Asn Tyr Gln Val Val His His Leu Phe Pro Ser Val Ser
                405                 410                 415

Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys
            420                 425                 430

Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe
            435                 440                 445

Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala
    450                 455                 460

Ala Thr Ile His Met Gly
465                 470

<210>   39
<211>   819
<212>   DNA
<213>   Thraustochytrium aureum

<400>   39
atggcaaaca gcagcgtgtg ggatgatgtg gtgggccgcg tggagaccgg cgtggaccag     60
tggatggatg gcgccaagcc gtacgcactc accgatgggc tcccgatgat ggacgtgtcc    120
accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg    180
aggcagatgg agaagccttt tgagctcaag accatcaagc tcttgcacaa cttgtttctc    240
ttcggacttt ccttgtacat gtgcgtggtg accatccgcc aggctatcct ggaggctac     300
aaagtgtttg aaacgacat ggagaagggc aacgagctc atgctcaggg catgtctcgc      360
atcgtgtacg tgttctacgt gtccaaggca tacgagttct tggataccgc catcatgatc    420
ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccattttt    480
gccatctggt gggctatcgc caagtacgct ccaggaggtg atgcgtactt ttcagtgatc    540
ctcaactctt tcgtgcacac cgtcatgtac gcatactact tcttctcctc ccaagggttc    600
gggttcgtga agccaatcaa gccgtacatc accacccttc agatgaccca gttcatggca    660
atgcttgtgc agtccttgta cgactacctc ttcccatgcg actacccaca ggctcttgtg    720
```

14

```
cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag    780
agctatctta aaaagccaaa aaagagcaag accaactaa                           819
```

<210> 40
<211> 272
<212> PRT
<213> Thraustochytrium aureum

<400> 40

```
Met Ala Asn Ser Ser Val Trp Asp Asp Val Val Gly Arg Val Glu Thr
1               5                   10                  15

Gly Val Asp Gln Trp Met Asp Gly Ala Lys Pro Tyr Ala Leu Thr Asp
            20                  25                  30

Gly Leu Pro Met Met Asp Val Ser Thr Met Leu Ala Phe Glu Val Gly
        35                  40                  45

Tyr Met Ala Met Leu Leu Phe Gly Ile Pro Ile Met Arg Gln Met Glu
    50                  55                  60

Lys Pro Phe Glu Leu Lys Thr Ile Lys Leu Leu His Asn Leu Phe Leu
65                  70                  75                  80

Phe Gly Leu Ser Leu Tyr Met Cys Val Val Thr Ile Arg Gln Ala Ile
                85                  90                  95

Leu Gly Gly Tyr Lys Val Phe Gly Asn Asp Met Glu Lys Gly Asn Glu
            100                 105                 110

Ser His Ala Gln Gly Met Ser Arg Ile Val Tyr Val Phe Tyr Val Ser
        115                 120                 125

Lys Ala Tyr Glu Phe Leu Asp Thr Ala Ile Met Ile Leu Cys Lys Lys
        130                 135                 140

Phe Asn Gln Val Ser Phe Leu His Val Tyr His His Ala Thr Ile Phe
145                 150                 155                 160

Ala Ile Trp Trp Ala Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr
                165                 170                 175

Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr
            180                 185                 190

Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro
        195                 200                 205

Tyr Ile Thr Thr Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln
    210                 215                 220

Ser Leu Tyr Asp Tyr Leu Phe Pro Cys Asp Tyr Pro Gln Ala Leu Val
225                 230                 235                 240

Gln Leu Leu Gly Val Tyr Met Ile Thr Leu Leu Ala Leu Phe Gly Asn
            245                 250                 255

Phe Phe Val Gln Ser Tyr Leu Lys Lys Pro Lys Lys Ser Lys Thr Asn
        260                 265                 270
```

15

<210> 41
<211> 1077
<212> DNA
<213> Saprolegnia diclina

<400> 41
atgactgagg ataagacgaa ggtcgagttc ccgacgctca cggagctcaa gcactcgatc   60
ccgaacgcgt gctttgagtc gaacctcggc ctctcgctct actacacggc ccgcgcgatc   120
ttcaacgcgt cggcctcggc ggcgctgctc tacgcggcgc gctcgacgcc gttcattgcc   180
gataacgttc tgctccacgc gctcgtttgc gccacctaca tctacgtgca gggcgtcatc   240
ttctggggct tcttcacggt cggccacgac tgcggccact cggccttctc gcgctaccac   300
agcgtcaact ttatcatcgg ctgcatcatg cactctgcga tttttgacgcc gttcgagagc   360
tggcgcgtga cgcaccgcca ccaccacaag aacacgggca acattgataa ggacgagatc   420
ttttacccgc accggtcggt caaggacctc caggacgtgc gccaatgggt ctacacgctc   480
ggcggtgcgt ggtttgtcta cttgaaggtc gggtatgccc cgcgcacgat gagccacttt   540
gacccgtggg acccgctcct ccttcgccgc gcgtcggccg tcatcgtgtc gctcggcgtc   600
tgggccgcct tcttcgccgc gtacgcgtac ctcacatact cgctcggctt tgccgtcatg   660
ggcctctact actatgcgcc gctctttgtc tttgcttcgt tcctcgtcat tacgaccttc   720
ttgcaccaca cgacgaagc gacgccgtgg tacggcgact cggagtggac gtacgtcaag   780
ggcaacctct cgagcgtcga ccgctcgtac ggcgcgttcg tggacaacct gagccaccac   840
attggcacgc accaggtcca ccacttgttc ccgatcattc cgcactacaa gctcaacgaa   900
gccaccaagc actttgcggc cgcgtacccg cacctcgtgc gcaggaacga cgagcccatc   960
atcacggcct tcttcaagac cgcgcacctc tttgtcaact acggcgctgt gcccgagacg   1020
gcgcagatct tcacgctcaa agagtcggcc gcggccgcca aggccaagtc ggactaa   1077

<210> 42
<211> 358
<212> PRT
<213> Saprolegnia diclina

<400> 42
Met Thr Glu Asp Lys Thr Lys Val Glu Phe Pro Thr Leu Thr Glu Leu
1   5   10   15

Lys His Ser Ile Pro Asn Ala Cys Phe Glu Ser Asn Leu Gly Leu Ser
            20   25   30

Leu Tyr Tyr Thr Ala Arg Ala Ile Phe Asn Ala Ser Ala Ser Ala Ala
        35   40   45

Leu Leu Tyr Ala Ala Arg Ser Thr Pro Phe Ile Ala Asp Asn Val Leu
    50   55   60

Leu His Ala Leu Val Cys Ala Thr Tyr Ile Tyr Val Gln Gly Val Ile
65   70   75   80

Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys Gly His Ser Ala Phe
                85   90   95

Ser Arg Tyr His Ser Val Asn Phe Ile Ile Gly Cys Ile Met His Ser
                100   105   110

Ala Ile Leu Thr Pro Phe Glu Ser Trp Arg Val Thr His Arg His His
            115   120   125

His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu Ile Phe Tyr Pro His
        130   135   140

Arg Ser Val Lys Asp Leu Gln Asp Val Arg Gln Trp Val Tyr Thr Leu
145   150   155   160

16

```
Gly Gly Ala Trp Phe Val Tyr Leu Lys Val Gly Tyr Ala Pro Arg Thr
            165                 170                 175

Met Ser His Phe Asp Pro Trp Asp Pro Leu Leu Leu Arg Arg Ala Ser
            180                 185                 190

Ala Val Ile Val Ser Leu Gly Val Trp Ala Ala Phe Phe Ala Ala Tyr
            195                 200                 205

Ala Tyr Leu Thr Tyr Ser Leu Gly Phe Ala Val Met Gly Leu Tyr Tyr
            210                 215                 220

Tyr Ala Pro Leu Phe Val Phe Ala Ser Phe Leu Val Ile Thr Thr Phe
225                     230                 235                 240

Leu His His Asn Asp Glu Ala Thr Pro Trp Tyr Gly Asp Ser Glu Trp
            245                 250                 255

Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala
            260                 265                 270

Phe Val Asp Asn Leu Ser His His Ile Gly Thr His Gln Val His His
            275                 280                 285

Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn Glu Ala Thr Lys His
            290                 295                 300

Phe Ala Ala Ala Tyr Pro His Leu Val Arg Arg Asn Asp Glu Pro Ile
305                     310                 315                 320

Ile Thr Ala Phe Phe Lys Thr Ala His Leu Phe Val Asn Tyr Gly Ala
            325                 330                 335

Val Pro Glu Thr Ala Gln Ile Phe Thr Leu Lys Glu Ser Ala Ala Ala
            340                 345                 350

Ala Lys Ala Lys Ser Asp
            355


<210>  43
<211>  957
<212>  DNA
<213>  Mortierella alpina

<400>  43
atggagtcga ttgcgccatt cctcccatca agatgccgc aagatctgtt tatggacctt      60
gccaccgcta tcggtgtccg ggccgcgccc tatgtcgatc ctctcgaggc cgcgctggtg     120
gcccaggccg agaagtacat ccccacgatt gtccatcaca cgcgtgggtt cctggtcgcg     180
gtggagtcgc ctttggcccg tgagctgccg ttgatgaacc cgttccacgt gctgttgatc     240
gtgctcgctt atttggtcac ggtctttgtg ggcatgcaga tcatgaagaa ctttgagcgg     300
ttcgaggtca agacgttttc gctcctgcac aacttttgtc tggtctcgat cagcgcctac     360
atgtgcggtg ggatcctgta cgaggcttat caggccaact atggactgtt tgagaacgct     420
gctgatcata ccttcaaggg tcttcctatg gccaagatga tctggctctt ctacttctcc     480
aagatcatgg agtttgtcga caccatgatc atggtcctca agaagaacaa ccgccagatc     540
tccttcttgc acgtttacca ccacagctcc atcttcacca tctggtggtt ggtcaccttt     600
gttgcaccca cggtgaagc ctacttctct gctgcgttga actcgttcat ccatgtgatc     660
atgtacggct actacttctt gtcggccttg ggcttcaagc aggtgtcgtt catcaagttc     720
tacatcacgc gctcgcagat gacacagttc tgcatgatgt cggtccagtc ttcctgggac     780
atgtacgcca tgaaggtcct tggccgcccc ggataccccct tcttcatcac ggctctgctt     840
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17

```
tggttctaca tgtggaccat gctcggtctc ttctacaact tttacagaaa gaacgccaag      900
ttggccaagc aggccaaggc cgacgctgcc aaggagaagg caaggaagtt gcagtaa         957


<210>  44
<211>  318
<212>  PRT
<213>  Mortierella alpina

<400>  44
Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu
1               5                   10                  15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val
            20                  25                  30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro
        35                  40                  45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro
    50                  55                  60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile
65                  70                  75                  80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys
                85                  90                  95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe
            100                 105                 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu
            115                 120                 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr
        130                 135                 140

Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser
145                 150                 155                 160

Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn
                165                 170                 175

Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe
            180                 185                 190

Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr
            195                 200                 205

Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr
    210                 215                 220

Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe
225                 230                 235                 240

Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln
                245                 250                 255

Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr
                260                 265                 270
```

18

```
Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu
        275             280              285

Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln
    290             295              300

Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln
305             310              315
```

<210> 45
<211> 1483
<212> DNA
<213> Mortierella alpina

<400> 45
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gcttcctcca gttcatcctc catttcgcca cctgcattct ttacgaccgt taagcaagat    60
gggaacggac caaggaaaaa ccttcacctg gaagagctg gcggcccata acaccaagga   120
cgacctactc ttggccatcc gcggcagggt gtacgatgtc acaaagttct tgagccgcca   180
tcctggtgga gtggacactc tcctgctcgg agctggccga gatgttactc cggtctttga   240
gatgtatcac gcgtttgggg ctgcagatgc cattatgaag aagtactatg tcggtacact   300
ggtctcgaat gagctgccca tcttcccgga gccaacggtg ttccacaaaa ccatcaagac   360
gagagtcgag ggctacttta cggatcggaa cattgatccc aagaatagac cagagatctg   420
gggacgatac gctcttatct ttggatcctt gatcgcttcc tactacgcgc agctctttgt   480
gcctttcgtt gtcgaacgca catggcttca ggtggtgttt gcaatcatca tgggatttgc   540
gtgcgcacaa gtcggactca accctcttca tgatgcgtct cacttttcag tgacccacaa   600
ccccactgtc tggaagattc tgggagccac gcacgacttt ttcaacggag catcgtacct   660
ggtgtggatg taccaacata tgctcggcca tcacccctac accaacattg ctggagcaga   720
tcccgacgtg tcgacgtctg agcccgatgt tcgtcgtatc aagcccaacc aaaagtggtt   780
tgtcaaccac atcaaccagc acatgtttgt tccttttcctg tacggactgc tggcgttcaa   840
ggtgcgcatt caggacatca acattttgta ctttgtcaag accaatgacg ctattcgtgt   900
caatcccatc tcgacatggc acactgtgat gttctggggc ggcaaggctt ctctttgtctg   960
gtatcgcctg attgttcccc tgcagtatct gcccctgggc aaggtgctgc tcttgttcac  1020
ggtcgcggac atggtgtcgt cttactggct ggcgctgacc ttccaggcga accacgttgt  1080
tgaggaagtt cagtggccgt tgcctgacga gaacgggatc atccaaaagg actgggcagc  1140
tatgcaggtc gagactacgc aggattacgc acacgattcg cacctctgga ccagcatcac  1200
tggcagcttg aactaccagg ctgtgcacca tctgttcccc aacgtgtcgc agcaccatta  1260
tcccgatatt ctggccatca tcaagaacac ctgcagcgag tacaaggttc cataccttgt  1320
caaggatacg ttttggcaag catttgcttc acatttggag cacttgcgtg ttcttggact  1380
ccgtcccaag gaagagtaga agaaaaaaag cgccgaatga agtattgccc ccttttttctc  1440
caagaatggc aaaaggagat caagtggaca ttctctatga aga                    1483
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<210> 46
<211> 446
<212> PRT
<213> Mortierella alpina

<400> 46
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Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala
1               5               10              15

His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr
            20              25              30

Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu
        35              40              45

Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His
    50              55              60
```

```
Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr
65              70              75                      80

Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His
            85              90                  95

Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile
            100             105             110

Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe
        115             120             125

Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val
    130             135             140

Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe
145             150             155             160

Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe
            165             170             175

Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His
            180             185             190

Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met
    195             200             205

Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val
    210             215             220

Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp
225             230             235             240

Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly
            245             250             255

Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe
            260             265             270

Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His
    275             280             285

Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu
    290             295             300

Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe
305             310             315             320

Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln
            325             330             335

Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn
            340             345             350

Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln
    355             360             365

Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu
    370             375             380
```

20

Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His
385   390   395   400

Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys
                405   410   415

Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His
            420   425   430

Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu
        435   440   445

<210>   47
<211>   1350
<212>   DNA
<213>   Arabidopsis thaliana

<400>   47
ctctctctct ctctcttctc tctttctctc cccctctctc cggcgatggt tgttgctatg   60
gaccaacgca ccaatgtgaa cggagatccc ggcgccggag accggaagaa agaagaaagg   120
tttgatccga gtgcacaacc accgttcaag atcggagata taagggcggc gattcctaag   180
cactgttggg ttaagagtcc tttgagatca atgagttacg tcgtcagaga cattatcgcc   240
gtcgcggctt tggccatcgc tgccgtgtat gttgatagct ggttcctttg gcctctttat   300
tgggccgccc aaggaacact tttctgggcc atctttgttc tcggccacga ctgtggacat   360
gggagtttct cagacattcc tctactgaat agtgtggttg gtcacattct tcattctttc   420
atcctcgttc cttaccatgg ttggagaata agccaccgga cacaccacca gaaccatggc   480
catgttgaaa cgacgagtc atgggttccg ttaccagaaa gggtgtacaa gaaattgccc   540
cacagtactc ggatgctcag atacactgtc cctctcccca tgctcgcata tcctctctat   600
ttgtgctaca gaagtcctgg aaaagaagga tcacatttta acccatacag tagtttattt   660
gctccaagcg agagaaagct tattgcaact tcaactactt gttggtccat aatgttcgtc   720
agtcttatcg ctctatcttt cgtcttcggt ccactcgcgg ttcttaaagt ctacggtgta   780
ccgtacatta tctttgtgat gtggttggat gctgtcacg atttgcatca tcatggtcac   840
gatgagaagt tgccttggta tagaggcaag gaatggagtt atctacgtgg aggattaaca   900
acaattgata gagattacgg aatctttaac aacattcatc acgacattgg aactcacgtg   960
atccatcatc tcttcccaca aatccctcac tatcacttgg tcgacgccac gaaagcagct 1020
aaacatgtgt tgggaagata ctacagagaa ccaaagacgt caggagcaat accgatccac 1080
ttggtggaga gtttggtcgc aagtattaag aaagatcatt acgtcagcga cactggtgat 1140
attgtcttct acgagacaga tccagatctc tacgtttacg cttctgacaa atctaaaatc 1200
aattaatctc catttgttta gctctattag gaataaacca gcccactttt aaaatttta   1260
tttcttgttg tttttaagtt aaaagtgtac tcgtgaaact cttttttttt tctttttttt 1320
tattaatgta tttacattac aaggcgtaaa   1350

<210>   48
<211>   386
<212>   PRT
<213>   Arabidopsis thaliana

<400>   48
Met Val Val Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly
1   5   10   15

Ala Gly Asp Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro
            20   25   30

Pro Phe Lys Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp
            35   40   45

Val Lys Ser Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile
    50   55   60

21

```
Ala Val Ala Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe
65              70              75              80

Leu Trp Pro Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile
                85              90              95

Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro
            100             105             110

Leu Leu Asn Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val
        115             120             125

Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His
    130             135             140

Gly His Val Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val
145             150             155             160

Tyr Lys Lys Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro
            165             170             175

Leu Pro Met Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly
            180             185             190

Lys Glu Gly Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser
    195             200             205

Glu Arg Lys Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe
    210             215             220

Val Ser Leu Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu
225             230             235             240

Lys Val Tyr Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala
            245             250             255

Val Thr Tyr Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr
            260             265             270

Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp
        275             280             285

Arg Asp Tyr Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His
    290             295             300

Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp
305             310             315             320

Ala Thr Lys Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro
            325             330             335

Lys Thr Ser Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala
        340             345             350

Ser Ile Lys Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe
        355             360             365

Tyr Glu Thr Asp Pro Asp Leu Tyr Val Tyr Ala Ser Asp Lys Ser Lys
    370             375             380
```

22

Ile Asn
385

<210> 49
<211> 834
<212> DNA
<213> Pavlova sp.

<400> 49
atgatgttgg ccgcaggcta tcttctagtg ctctcggccg ctcgccagag cttccagcag   60
gacattgaca accccaacgg ggcctactcg acctcgtgga ctggcctgcc cattgtgatg   120
tctgtggtct atctcagcgg tgtgtttggg ctcacaaagt acttcgagaa ccggaagccc   180
atgacggggc tgaaggacta catgttcact acaatctct accaggtgat catcaacgtg   240
tggtgcgtgg tggcctttct cctggaggtg cggcgtgcgg gcatgtcact catcggcaat   300
aaggtggacc ttgggcccaa ctccttcagg ctcggcttcg tcacgtgggt gcactacaac   360
aacaagtacg tggagctcct cgacaccta tggatggtgc tgcgcaagaa gacgcagcag   420
gtctccttcc tccacgtcta tcatcacgtg cttctgatgt gggcctggtt cgttgtcgtc   480
aagctcggca atggtggtga cgcatatttt ggcggtctca tgaactcgat catccacgtg   540
atgatgtatt cctactacac catggcgctc ctgggctggt catgcccctg gaagcgctac   600
ctcacgcagg cacagctcgt gcagtttgc atctgcctcg cccactccac atgggcggca   660
gtaacgggtg cctaccgtg gcgaatttgc ttggtggagg tgtgggtgat ggtgtccatg   720
ctggtgctct tcacacgctt ctaccgccag gcctatgcca aggaggcgaa ggccaaggag   780
gcgaaaaagc tcgcacagga ggcatcacag gccaaggcgg tcaaggcgga gtaa   834

<210> 50
<211> 277
<212> PRT
<213> Pavlova sp.

<400> 50
Met Met Leu Ala Ala Gly Tyr Leu Leu Val Leu Ser Ala Ala Arg Gln
1   5   10   15

Ser Phe Gln Gln Asp Ile Asp Asn Pro Asn Gly Ala Tyr Ser Thr Ser
            20   25   30

Trp Thr Gly Leu Pro Ile Val Met Ser Val Val Tyr Leu Ser Gly Val
            35   40   45

Phe Gly Leu Thr Lys Tyr Phe Glu Asn Arg Lys Pro Met Thr Gly Leu
    50   55   60

Lys Asp Tyr Met Phe Thr Tyr Asn Leu Tyr Gln Val Ile Ile Asn Val
65   70   75   80

Trp Cys Val Val Ala Phe Leu Leu Glu Val Arg Arg Ala Gly Met Ser
                85   90   95

Leu Ile Gly Asn Lys Val Asp Leu Gly Pro Asn Ser Phe Arg Leu Gly
            100   105   110

Phe Val Thr Trp Val His Tyr Asn Asn Lys Tyr Val Glu Leu Leu Asp
            115   120   125

Thr Leu Trp Met Val Leu Arg Lys Lys Thr Gln Gln Val Ser Phe Leu
        130   135   140

His Val Tyr His His Val Leu Leu Met Trp Ala Trp Phe Val Val Val
145   150   155   160

23

Lys Leu Gly Asn Gly Gly Asp Ala Tyr Phe Gly Gly Leu Met Asn Ser
              165   170   175

Ile Ile His Val Met Met Tyr Ser Tyr Tyr Thr Met Ala Leu Leu Gly
         180   185   190

Trp Ser Cys Pro Trp Lys Arg Tyr Leu Thr Gln Ala Gln Leu Val Gln
     195   200   205

Phe Cys Ile Cys Leu Ala His Ser Thr Trp Ala Ala Val Thr Gly Ala
   210   215   220

Tyr Pro Trp Arg Ile Cys Leu Val Glu Val Trp Val Met Val Ser Met
225   230   235   240

Leu Val Leu Phe Thr Arg Phe Tyr Arg Gln Ala Tyr Ala Lys Glu Ala
         245   250   255

Lys Ala Lys Glu Ala Lys Lys Leu Ala Gln Glu Ala Ser Gln Ala Lys
         260   265   270

Ala Val Lys Ala Glu
         275

<210> 51
<211> 1530
<212> DNA
<213> Schizochytrium aggregatum

<400> 51
atgacggtgg gcggcgatga ggtgtacagc atggcgcagg tgcgcgacca caacaccccg   60
gacgacgcct ggtgcgccat ccacggcgag gtgtacgagc tgaccaagtt cgcccgcacc   120
caccccgggg gggacatcat cttgctggcc gccggcaagg aggccaccat cctgttcgag   180
acgtaccacg tgcgccccat ctccgacgcg gtcctgcgca agtaccgcat cggcaagctc   240
gccgccgccg gcaaggatga gccggccaac gacagcacct actacagctg ggacagcgac   300
ttttacaagg tgctccgcca gcgtgtcgtg gcgcgcctcg aggagcgcaa gatcgcccgc   360
cgcggcggcc ccgagatctg gatcaaggcc gccatcctcg tcagcggctt ctggtccatg   420
ctctacctca tgtgcaccct ggacccgaac cgcggcgcca tcctggccgc catcgcgctg   480
ggcatcgtcg ccgccttcgt cggcacgtgc attcagcacg acggcaacca cggcgcgttc   540
gccttctctc cgttcatgaa caagctctct ggctggacgc tcgacatgat cggcgccagt   600
gccatgacct gggagatgca gcacgtgctg ggccaccacc cgtacaccaa cctgatcgag   660
atggagaacg gcacccaaaa ggtcacccac gccgacgtcg accccaagaa ggccgaccag   720
gagagcgacc cggacgtctt cagcacctac cccatgctcc gtctgcaccc gtggcaccgc   780
aagcgcttct accaccgctt ccagcacctg tacgcgccgc tgctcttcgg tttcatgacc   840
atcaacaagg tgatcaccca ggatgtggga gttgtcctca gcaagcgtct gtttcagatc   900
gatgccaact gccgttacgc cagcaagtcg tacgttgcgc gcttctggat catgaagctg   960
ctcaccgtcc tctacatggt cgccctcccc gtgtacaccc agggccttgt cgacgggctc   1020
aagctcttct tcatcgccca cttttcgtgc ggcgagctgc tggccaccat gttcatcgtc   1080
aaccacatca tcgagggcgt ctcgtacgcc tccaaggact ctgtcaaggg caccatggcg   1140
ccgccgcgca cggtgcacgg cgtgaccccg atgcatgaca cccgcgacgc gctcggcaag   1200
gagaaggcag ccaccaagca cgtgccgctc aacgactggg ccgcggtcca gtgccagacc   1260
tcggtcaact ggtcgatcgg ctcgtggttc tggaaccact tctccggcgg gctcaaccac   1320
cagatcgagc accacctctt ccccggcctc acccacacca cctacgtgta cattcaggat   1380
gtggtgcagg cgacgtgcgc cgagtacggg gtcccgtacc agtcggagca gagcctcttc   1440
tccgcctact tcaagatgct ctcccacctt cgggcgctcg caacgagcc gatgccctcg   1500
tgggagaagg accaccccaa gtccaagtga   1530

<210> 52
<211> 509

24

<212> PRT
<213> Schizochytrium aggregatum

<400> 52
Met Thr Val Gly Gly Asp Glu Val Tyr Ser Met Ala Gln Val Arg Asp
1   5   10   15

His Asn Thr Pro Asp Asp Ala Trp Cys Ala Ile His Gly Glu Val Tyr
            20   25   30

Glu Leu Thr Lys Phe Ala Arg Thr His Pro Gly Gly Asp Ile Ile Leu
        35   40   45

Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Val
    50   55   60

Arg Pro Ile Ser Asp Ala Val Leu Arg Lys Tyr Arg Ile Gly Lys Leu
65   70   75   80

Ala Ala Ala Gly Lys Asp Glu Pro Ala Asn Asp Ser Thr Tyr Tyr Ser
                85   90   95

Trp Asp Ser Asp Phe Tyr Lys Val Leu Arg Gln Arg Val Val Ala Arg
            100   105   110

Leu Glu Glu Arg Lys Ile Ala Arg Arg Gly Gly Pro Glu Ile Trp Ile
        115   120   125

Lys Ala Ala Ile Leu Val Ser Gly Phe Trp Ser Met Leu Tyr Leu Met
    130   135   140

Cys Thr Leu Asp Pro Asn Arg Gly Ala Ile Leu Ala Ala Ile Ala Leu
145   150   155   160

Gly Ile Val Ala Ala Phe Val Gly Thr Cys Ile Gln His Asp Gly Asn
                165   170   175

His Gly Ala Phe Ala Phe Ser Pro Phe Met Asn Lys Leu Ser Gly Trp
            180   185   190

Thr Leu Asp Met Ile Gly Ala Ser Ala Met Thr Trp Glu Met Gln His
        195   200   205

Val Leu Gly His His Pro Tyr Thr Asn Leu Ile Glu Met Glu Asn Gly
    210   215   220

Thr Gln Lys Val Thr His Ala Asp Val Asp Pro Lys Lys Ala Asp Gln
225   230   235   240

Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr Pro Met Leu Arg Leu His
            245   250   255

Pro Trp His Arg Lys Arg Phe Tyr His Arg Phe Gln His Leu Tyr Ala
            260   265   270

Pro Leu Leu Phe Gly Phe Met Thr Ile Asn Lys Val Ile Thr Gln Asp
        275   280   285

Val Gly Val Val Leu Ser Lys Arg Leu Phe Gln Ile Asp Ala Asn Cys
    290   295   300

25

```
Arg Tyr Ala Ser Lys Ser Tyr Val Ala Arg Phe Trp Ile Met Lys Leu
305              310              315              320

Leu Thr Val Leu Tyr Met Val Ala Leu Pro Val Tyr Thr Gln Gly Leu
             325              330              335

Val Asp Gly Leu Lys Leu Phe Phe Ile Ala His Phe Ser Cys Gly Glu
         340              345              350

Leu Leu Ala Thr Met Phe Ile Val Asn His Ile Ile Glu Gly Val Ser
         355              360              365

Tyr Ala Ser Lys Asp Ser Val Lys Gly Thr Met Ala Pro Pro Arg Thr
    370              375              380

Val His Gly Val Thr Pro Met His Asp Thr Arg Asp Ala Leu Gly Lys
385              390              395              400

Glu Lys Ala Ala Thr Lys His Val Pro Leu Asn Asp Trp Ala Ala Val
             405              410              415

Gln Cys Gln Thr Ser Val Asn Trp Ser Ile Gly Ser Trp Phe Trp Asn
         420              425              430

His Phe Ser Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro
         435              440              445

Gly Leu Thr His Thr Thr Tyr Val Tyr Ile Gln Asp Val Val Gln Ala
    450              455              460

Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu Gln Ser Leu Phe
465              470              475              480

Ser Ala Tyr Phe Lys Met Leu Ser His Leu Arg Ala Leu Gly Asn Glu
             485              490              495

Pro Met Pro Ser Trp Glu Lys Asp His Pro Lys Ser Lys
         500              505
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<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 53
gcggccgcat gactgaggat aagacga   27

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

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<400>   54
gcggccgctt agtccgactt ggccttg                                                        27

<210>   55
<211>   24
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   55
gcggccgcat ggagtcgatt gcgc                                                           24

<210>   56
<211>   24
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   56
gcggccgctt actgcaactt cctt                                                           24

<210>   57
<211>   24
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   57
gcggccgcat gggaacggac caag                                                           24

<210>   58
<211>   24
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   58
gcggccgcct actcttcctt ggga                                                           24

<210>   59
<211>   29
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   59
ttcctgcagg ctagcctaag tacgtactc                                                      29

<210>   60
<211>   21
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27

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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   60
aagcggccgc ggtgatgact g                                                    21

<210>   61
<211>   12
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus peptide

<400>   61
Thr Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys
1               5                   10

<210>   62
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<400>   62
atccgcgccg ccatccccaa gcactgctgg gtcaag                                    36

<210>   63
<211>   15
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus peptide

<400>   63
Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1               5                   10                  15

<210>   64
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (21)..(21)
<223>   y = c or t

<220>
<221>   unsure
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28

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<222>   (33)..(33)
<223>   y = c or t

<400>   64
gccctcttcg tcctcggcca ygactgcggc cayggctcgt tctcg                        45

<210>   65
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (4)..(4)
<223>   r = a or g

<220>
<221>   unsure
<222>   (10)..(10)
<223>   r = a or g

<220>
<221>   unsure
<222>   (30)..(30)
<223>   r = a or g

<220>
<221>   unsure
<222>   (31)..(31)
<223>   r = a or g

<220>
<221>   unsure
<222>   (34)..(34)
<223>   r = a or g

<220>
<221>   unsure
<222>   (38)..(38)
<223>   r = a or g

<220>
<221>   unsure
<222>   (39)..(39)
<223>   y = c or t

<220>
<221>   unsure
<222>   (43)..(43)
<223>   r = a or g

<400>   65
gagrtggtar tggggatct ggggaagar rtgrtggryg acrtg                         45

<210>   66
<211>   15
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<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus peptide

<400>   66
Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn
1                   5                   10                  15

<210>   67
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (9)..(9)
<223>   y = c or t

<220>
<221>   unsure
<222>   (27)..(27)
<223>   y = c or t

<220>
<221>   unsure
<222>   (36)..(36)
<223>   y = c or t

<220>
<221>   unsure
<222>   (39)..(39)
<223>   y = c or t

<400>   67
ccctaccayg gctggcgcat ctcgcaycgc acccaycayc agaac                45

<210>   68
<211>   45
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (7)..(7)
<223>   r = a or g

<220>
<221>   unsure
<222>   (10)..(10)
<223>   r = a or g
```

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<220>
<221>  unsure
<222>  (19)..(19)
<223>  r = a or g

<220>
<221>  unsure
<222>  (37)..(37)
<223>  r = a or g

<400>  68
gttctgrtgr tgggtccgrt gcgagatgcg ccagccrtgg taggg                    45

<210>  69
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  consensus peptide

<220>
<221>  UNSURE
<222>  (5)..(5)
<223>  Xaa = Asp or His

<220>
<221>  UNSURE
<222>  (7)..(7)
<223>  Xaa = Asp or Tyr

<400>  69
Gly Ser His Phe Xaa Pro Xaa Ser Asp Leu Phe Val
1               5                   10

<210>  70
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  synthetic oligonucleotide

<220>
<221>  unsure
<222>  (13)..(13)
<223>  s = c or g

<220>
<221>  unsure
<222>  (19)..(19)
<223>  k = g or t

<400>  70
ggctcgcact tcsacccka ctcggacctc ttcgtc                               36

<210>  71
<211>  36
<212>  DNA
<213>  Artificial Sequence
```

31

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<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (18)..(18)
<223>   m = a or c

<220>
<221>   unsure
<222>   (24)..(24)
<223>   w = a or t

<400>   71
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc                                 36

<210>   72
<211>   13
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus peptide

<220>
<221>   UNSURE
<222>   (3)..(3)
<223>   Xaa = Tyr or Phe

<220>
<221>   UNSURE
<222>   (4)..(4)
<223>   Xaa = Leu or Val

<220>
<221>   UNSURE
<222>   (11)..(11)
<223>   Xaa = Leu or Ile

<400>   72
Trp Ser Xaa Xaa Arg Gly Gly Leu Thr Thr Xaa Asp Arg
1               5                   10

<210>   73
<211>   39
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   synthetic oligonucleotide

<220>
<221>   unsure
<222>   (9)..(9)
<223>   k = g or t

<220>
<221>   unsure
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<222>  (30)..(30)
<223>  w = a or t

<220>
<221>  unsure
<222>  (32)..(32)
<223>  s = c or g

<400>  73
gcgctggakg gtggtgaggc cgccgcggaw gsacgacca                              39

<210>  74
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  consensus peptide

<400>  74
His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln
1               5                   10                  15

<210>  75
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  synthetic oligonucleotide

<220>
<221>  unsure
<222>  (13)..(13)
<223>  r = a or g

<220>
<221>  unsure
<222>  (16)..(16)
<223>  r = a or g

<220>
<221>  unsure
<222>  (25)..(25)
<223>  r = a or g

<220>
<221>  unsure
<222>  (40)..(40)
<223>  r = a or g

<220>
<221>  unsure
<222>  (43)..(43)
<223>  r = a or g

<400>  75
ctgggggaag agrtgrtgga tgacrtgggt gccgatgtcr tgrtg                       45
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<210>  76
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<220>
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<220>
<221>  UNSURE
<222>  (2)..(2)
<223>  Xaa = Leu or Phe

<220>
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<222>  (5)..(5)
<223>  Xaa = Gln or Lys

<220>
<221>  UNSURE
<222>  (12)..(12)
<223>  Xaa = Val or Ile

<400>  76
His Xaa Phe Pro Xaa Ile Pro His Tyr His Leu Xaa Glu Ala Thr
1               5                   10                  15

<210>  77
<211>  45
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<220>
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<220>
<221>  unsure
<222>  (12)..(12)
<223>  y = c or t

<220>
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<222>  (16)..(16)
<223>  r = a or g

<220>
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<222>  (22)..(22)
<223>  r = a or g

<220>
<221>  unsure
<222>  (33)..(33)
<223>  k = g or t

<220>
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<222>  (42)..(42)
<223>  r = a or g
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34

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<220>
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<222>  (43)..(43)
<223>  r = a or g

<400>  77
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<210>  78
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
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<220>
<221>  UNSURE
<222>  (3)..(3)
<223>  Xaa = Ala or Ile

<220>
<221>  UNSURE
<222>  (6)..(6)
<223>  Xaa = Leu or Phe

<400>  78
His Val Xaa His His Xaa Phe Pro Gln Ile Pro His Tyr His Leu
1               5                   10                  15

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<400>  79
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<210>  80
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<220>
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<400>  80
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<210>  81
<211>  25
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<400> 81
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<210> 82
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<220>
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<400> 82
tcaagggcaa cctctcgagc gtcgac   26

<210> 83
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<400> 83
cccagtcacg acgttgtaaa acgacggcca g   31

<210> 84
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<400> 85
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<210> 86
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<400> 86
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<210> 87
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36

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<400> 87
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<210> 88
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<210> 89
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<400> 89
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<210> 90
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taaatattaa tcattatttt taagatatta attaagaaat taaaagattt tttaaaaaaa   180
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tttttaattt cttaaaaaat gttgcaagac acttattaga catagtcttg ttctgtttac   300
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37

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<210> 92
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38

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<210> 93
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<210> 94
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